

09424347 Results

SEQ ID NO: 2

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	2924	100.0	563	20	AAW88489	Human organic anion
2	2832.5	96.9	550	21	AY44278	Human organic anion
3	2832.5	96.9	550	22	AAB47271	HOAT1. Homo sapie
4	2532	86.6	551	20	AAW88488	Rat organic anion
5	2457	84.0	545	22	AAB36553	Mouse organic anion
6	1410.5	48.2	542	22	AAB47274	HOAT3. Homo sapie
7	1409.5	48.2	542	21	AY92902	Human cerebral org
8	1369	46.8	561	18	AAW44196	Human osteoclast t
9	1368.5	46.8	537	18	AAW44195	Mouse osteoclast t
10	1366.5	46.7	536	21	AY92903	Rat cerebral organ
11	1225.5	41.9	553	22	AAE10332	Human transporter
12	1206	41.2	578	22	AAE06571	Human protein havi
13	1206	41.2	815	22	ABG26899	Novel human diagno
14	1127	38.5	550	22	AAE06612	Human protein havi
15	1127	38.5	550	22	AAB69091	Human organic anion
16	1115	38.1	566	22	AAE10336	Human transporter
17	1058.5	36.2	541	22	AAB47276	HOAT5. Homo sapie
18	996	34.1	535	21	AY51249	Rat liver anion tr

RESULT 1

AAW88489

ID AAW88489 standard; Protein; 563 AA.

XX

AC AAW88489;

XX

DT 05-MAR-1999 (first entry)

XX

DE Human organic anion transporter OAT-1.

XX

KW Organic anion transporter; OAT-1; nephrotoxicity; drug release; drug-drug interaction mechanism; drug elimination; kidney; beta-lactam antibiotic; non-steroidal antiinflammatory; diuretic.

XX

OS Homo sapiens.

XX

PN WO9853064-A1.

XX

PD 26-NOV-1998.

XX

PF 18-MAY-1998; 98WO-JP02171.

XX

PR 23-MAY-1997; 97JP-0134182.

XX

PA (TANA) TANABE SEIYAKU CO.

XX

PI Endou H, Hosoyamada M, Kanai Y, Sekine T;

XX

DR WPI; 1999-045310/04.

DR N-PSDB; AAV79585.

XX

PT New renal organic anion transporter protein - useful for, e.g.

PT screening potential drugs for prevention of nephrotoxicity and as a reagent for the investigation of drug metabolism

XX

PS Claim 1; Page 27-32; 45pp; Japanese.

XX

CC The present sequence represents human organic anion transporter protein

CC OAT-1. OAT-1 may be used as a reagent for the in vitro analysis and

CC study of drug release and drug-drug interaction mechanisms and drug

CC elimination via the kidney (e.g. for drugs such as beta-lactam

CC antibiotics, non-steroidal antiinflammatories and diuretics), and as

CC a reagent for screening candidate drugs for the prevention of
CC nephrotoxicity. Oligonucleotide sequences which hybridise to the OAT-1
CC polynucleotide may be used as probes for detection of OAT-1 gene
CC sequences.

XX

SQ Sequence 563 AA;

Query Match 100.0%; Score 2924; DB 20; Length 563;
Best Local Similarity 100.0%; Pred. No. 7.2e-290;
Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFNDLLQQVGGVGRFQQIQVTLVVPLLLLMA SHNTLQNF TAAIPTHHCRPPADANLSKN 60
Db 1 mafndl lqqvggvgrfqqiqvtlvvlp lllmashntlqnftaaipthhcrppad anlskn 60

Qy 61 GGLEVWLPRDRQQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI 120
Db 61 gglevw lprdrqqp escl rftspq wglp flngteangt gatepctdgwi ydnstfpsti 120

Qy 121 VTEWDLVCSH RALRQLAQS LYMG VGLL GAMVFGYLA DR LGRRKVL LILNYLQTA VSGTCAA 180
Db 121 vte wdlv csh ralrqlaqs lymg vgl lgamvfgyladr lgrrkvl llnylqta vsgtcaa 180

Qy 181 FAPNFPIYCAF RLLSGM ALAGISL NCMTL NV EWMPIH TRACVG TLIGYVYSLGQFLLAGV 240
Db 181 fapnfpiycafrllsgmalagisln cmtlnve wmpihtracvgtligyvyslgqfllagv 240

Qy 241 AYAVPHWRHLQ LLSVAPFFAFFIY SWFFIESARWHSSSGR LDTL RALQRVARINGKREE 300
Db 241 ayavphwrhlql lvsapffaffiy swffiesarwhsssgr ldtlralqrvar ingkree 300

Qy 301 GAKLSMEVLRASLQ KELTMGKGQASAME LLRCPTL RHLFLCLSM LWFAT SFAYYGLVMDL 360
Db 301 gaklsmev lraslq keltmgkgqasamellrcptl rhlflclsm lwfatsfayyglvmdl 360

Qy 361 QGFGVSIYLIQVIFGAVDLPAKLVGFLVINS LGRPAQMA ALLL AGICILLNGVIPQDQS 420
Db 361 qgfgvsiyliqvi fgavd lpa klg flv ins lgrpaqma alll agicillngvi p qdqs 420

Qy 421 IVRTSLAVLGKGCL AASFNCI FLYTGE LYPTMIR QTGMGMGST MARVGSIVSPLVSMTAE 480
Db 421 ivrt slavlgkgc laasfnciflytge lyptmir qtgm gmgst marvgsivs plvsmtae 480

Qy 481 LYP SMPLFIYGA VPVA ASAVT VILLE P T L G Q P L P D T V Q D L E S R W A P T Q K E A G I Y P R K G K Q T 540
Db 481 lyp smplfiyga vpva asavt vllpetlgqplpd tvqdlesrwaptqkeagiyp rkgkqt 540

Qy 541 RQQQE HQKYM VP LQAS A Q E K N G L 563
Db 541 rqqqehqkymvp lqas aqekngl 563

RESULT 4

AAW88488

ID AAW88488 standard; Protein; 551 AA.

XX

AC AAW88488;

XX

DT 05-MAR-1999 (first entry)

XX

DE Rat organic anion transporter OAT-1.

XX

KW Organic anion transporter; OAT-1; nephrotoxicity; drug release;
KW drug-drug interaction mechanism; drug elimination; kidney;
KW beta-lactam antibiotic; non-steroidal antiinflammatory; diuretic.

XX

OS Rattus sp.

XX

PN WO9853064-A1.

XX
PD 26-NOV-1998.
XX
PF 18-MAY-1998; 98WO-JP02171.
XX
PR 23-MAY-1997; 97JP-0134182.
XX
PA (TANA) TANABE SEIYAKU CO.
XX
PI Endou H, Hosoyamada M, Kanai Y, Sekine T;
XX
DR WPI; 1999-045310/04.
DR N-PSDB; AAV79584.
XX
PT New renal organic anion transporter protein - useful for, e.g.
PT screening potential drugs for prevention of nephrotoxicity and as a
PT reagent for the investigation of drug metabolism
XX
PS Claim 1; Page 22-26; 45pp; Japanese.
XX
CC The present sequence represents rat organic anion transporter protein
CC OAT-1. OAT-1 may be used as a reagent for the in vitro analysis and
CC study of drug release and drug-drug interaction mechanisms and drug
CC elimination via the kidney (e.g. for drugs such as beta-lactam
CC antibiotics, non-steroidal antiinflammatories and diuretics), and as
CC a reagent for screening candidate drugs for the prevention of
CC nephrotoxicity. Oligonucleotide sequences which hybridise to the OAT-1
CC polynucleotide may be used as probes for detection of OAT-1 gene
CC sequences.
XX
SQ Sequence 551 AA;

Query Match 86.6%; Score 2532; DB 20; Length 551;
Best Local Similarity 85.6%; Pred. No. 8.6e-250;
Matches 482; Conservative 35; Mismatches 34; Indels 12; Gaps 1;

Qy 1 MAFNDLLQQVGGVGRFQQIQVTLVVLPLLLMASHNTLQNFTAAIPTHHCRRPPADANLSKN 60
Db 1 mafndl1kqvgvgvgrfqlqvtmvavpl1lmashtlqnftaaipp hhcrppananlskd 60

Qy 61 GGLEVWLPRDRQGPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI 120
Db 61 ggleawlp1dkqggpescrlftspqwgppfyngteangtrvtepcidgwvydnstlpsti 120

Qy 121 VTEWLVCSSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLLNYLQTAVSGTCAA 180
Db 121 vtewnlvcshrafrqlaqsllymgvllgamvfgyladrlgrrkvllnylqtavsgtcaa 180

Qy 181 FAPNFPIYCAFRLLSGMALAGISLNCMTLNVEWMPHIHTRACVGTLIGYVYSLGQFLLAGV 240
Db 181 yapnytvycvfrllsgmsasiaincmtlnvewmpihtrayvgtligyvyslgqfllagi 240

Qy 241 AYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSGRDLTLRALQRVARINGKREE 300
Db 241 ayavphwrhlqlvvsvpffiafiyswffiesarwyssgrldltlralqrvaringkree 300

Qy 301 GAKLSMEVLRASLQKELTMKGQASAMELLRCPTLRLFLCLSMWFATSFAYYGLVMDL 360
Db 301 gaklsievrlrtslqkeltlsgqasamellrcptirhlfclsmiwfatsfayyglvmdl 360

Qy 361 QGFGVSIYLIQVIFGAVDLPACKLVGFLVINSLGRRPAQMAALLLAGICILLNGVIPQDQS 420
Db 361 qgfgvsmlyliqvifgavdlpakfvclfvinsmgrrpaqmasllagicalvngiipksht 420

Qy 421 IVRTSLAVLGKGCLAASFNCIFLYTGEELYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480
Db 421 iirtslavlgkgclassfncciflytgeelyptvirqtglmgstmarvgsivsplvrmtae 480

Qy 481 LYPSMPLIFIYGAVPVAASAVTLLPETLGQPLPDTVQDLESRWAQKAEAGIYPRKGKQT 540
Db 481 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 481 fyppsmplifgavpvvasavtallpetlgqplpdvqdlksr-----srgkqn 528
Qy 541 RQQQEHQKYMVPLQASAQEKNGL 563
:||||| || :||||| |||||||
Db 529 qqqqeqqkqmmplqastqekngl 551

RESULT 9
AAW44195
ID AAW44195 standard; Protein; 537 AA.
XX
AC AAW44195;
XX
DT 14-MAY-1998 (first entry)
XX
DE Mouse osteoclast transporter protein.
XX
KW Mouse; osteoclast transporter protein; osteoporosis; osteopetrosis.
XX
OS Mus musculus.
XX
PN WO9742321-A1.
XX
PD 13-NOV-1997.
XX
PF 09-MAY-1997; 97WO-US07856.
XX
PR 09-MAY-1996; 96US-0647397.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Beier DR, Brady KP;
XX
DR WPI; 1997-558983/51.
DR N-PSDB; AAV12391.
XX
PT Novel human and mouse osteoclast transporter proteins - useful for
PT isolating agents that decrease osteoclast activity, for treatment of
PT osteoporosis and osteopetrosis
XX
PS Disclosure; Page 26-29; 52pp; English.
XX
CC The present sequence represents mouse osteoclast transporter protein.
CC Agents that bind the nucleic acid encoding the osteoclast transporter
CC protein can be used to decrease its expression, thereby decreasing
CC osteoclast activity. The agents can be used to treat osteoporosis
CC and osteopetrosis.
XX
SQ Sequence 537 AA;

Qy 239 GVAYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSGRLDLTLRALQVARINGKR 298
 :||||| ||||| ||| : ||: ||| ||: ||: ||| ||| :
 Db 227 glayavpqwrwlqlsvsaaffifslswwvpesirwlvlsgrksralktlqrvatfngkk 286
 Qy 299 EEGAKLMSMEVLRASLQKELTMGKGQASAMELLRCPTLRHFLCLSMWFATSFAYYGLVM 358
 ||| ||:::| : :||:::| : :| | || : |||: ||| ||| ||| :
 Db 287 eegekltveelkfnlqkditsakvkyglSDLfrvsilrrvtfcslawfatgfayysslam 346
 Qy 359 DLQGFGVSIYLIQVIFGAVDLPALKVGLVINSLGRRPAQMAALLLAGICILLNGVIPQD 418
 :: |||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 347 gveefgvniyilqiifggvdipakfitilsisylgrritqgffllilagvailalifvsse 406
 Qy 419 QSVIRTSЛАVLGKGCLAAFSNCIFLYTGELEYPTMIRQTGMGMGSTMARVGSIVSPLVSMT 478
 ::||:||| |||||: ||:||| |||||:||:||| |||||:||:||| :|||:||| :|||:
 Db 407 mqllrtalavfgkgclsgsfscflytselyptvrlrqtmqgisniwarvgsmiaplvkit 466
 Qy 479 AELYPSMPLFIYGAJVVAASAVTLLPETLGQPLPDTVQDLESRWAPTQKEAGIYPRKGK 538
 ||| | :| | : :| :| | ||| :||:||:||:| :| | |
 Db 467 gelqfpipnvnifwtmtllggsaafflletlnrplpetiediqdwyqqt-----k 515
 Qy 539 QTRQQQEHQK--YMVPLQ 554
 :|:|:| :| :| :||:
 Db 516 ktkqepeaekasqtiplk 533

Issued:

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1368.5	46.8	537	2	US-08-647-397-2	Sequence 2, Appli
2	701.5	24.0	556	3	US-08-501-572-1	Sequence 1, Appli
3	701.5	24.0	556	3	US-09-040-444-1	Sequence 1, Appli
4	700	23.9	555	3	US-08-501-572-3	Sequence 3, Appli
5	700	23.9	555	3	US-09-040-444-3	Sequence 3, Appli
6	670	22.9	553	3	US-08-501-572-2	Sequence 2, Appli
7	670	22.9	553	3	US-09-040-444-2	Sequence 2, Appli
8	344	11.8	520	4	US-08-964-127-2	Sequence 2, Appli
9	344	11.8	520	4	US-09-496-692-2	Sequence 2, Appli
10	292	10.0	109	2	US-08-647-397-4	Sequence 4, Appli
11	244.5	8.4	286	4	US-08-964-127-4	Sequence 4, Appli
12	244.5	8.4	286	4	US-09-496-692-4	Sequence 4, Appli
13	200.5	6.9	322	4	US-08-964-127-6	Sequence 6, Appli
14	200.5	6.9	322	4	US-09-496-692-6	Sequence 6, Appli
15	200.5	6.9	563	2	US-09-031-392-2	Sequence 2, Appli

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	720.5	24.6	593	2	JC4884	organic cation tra
2	706.5	24.2	556	2	S50862	organic cation tra
3	655	22.4	576	2	T22509	hypothetical prote
4	628	21.5	557	2	JW0089	organic cation tra
5	613	21.0	557	2	JE0346	high-affinity carn
6	457	15.6	745	2	T16565	hypothetical prote
7	450.5	15.4	794	2	T27870	hypothetical prote
8	429.5	14.7	539	2	C96758	probable protein
9	408.5	14.0	515	2	B96825	hypothetical prote
10	401.5	13.7	527	2	T01019	transport protein
11	395.5	13.5	447	2	D89646	protein ZK455.8 [i]

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	628	21.5	557	1	OCN2_HUMAN	Q76082 homo sapien
2	626	21.4	557	1	OCN2_MOUSE	Q9z0e8 mus musculu
3	626	21.4	557	1	OCN2_RAT	Q70594 rattus norv
4	387	13.2	529	1	Y0U1_CAEEL	P30638 caenorhabdi
5	334	11.4	751	1	YLX5_CAEEL	P46501 caenorhabdi
6	275	9.4	435	1	YT13_CAEEL	Q10917 caenorhabdi
7	261	8.9	400	1	YCE1_BACSU	Q34691 bacillus su
8	260.5	8.9	482	1	YFIG_BACSU	P54723 bacillus su
9	240.5	8.2	445	1	YGCS_ECOLI	Q46909 escherichia
10	239.5	8.2	742	1	SYV2_RAT	Q02563 rattus norv
11	239	8.2	1222	1	YMP3_CAEEL	Q10947 caenorhabdi
12	229	7.8	451	1	YYAJ_BACSU	P37514 bacillus su

RESULT 4

Y0U1_CAEEL

ID Y0U1_CAEEL STANDARD; PRT; 529 AA.

AC P30638; Q21101;

DT 01-APR-1993 (Rel. 25, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Hypothetical 58.3 kDa protein ZK637.1 in chromosome III.

GN ZK637.1.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;

RX MEDLINE=92168156; PubMed=1538779;

RA Sulston J., Du Z., Thomas K., Wilson R., Hillier L., Staden R.,

RA Halloran N., Green P., Thierry-Mieg J., Qiu L., Dear S., Coulson A.,

RA Craxton M., Durbin R.K., Berks M., Metzstein M., Hawkins T.,

RA Ainscough R., Waterston R.;

RT "The C. elegans genome sequencing project: a beginning.";

RL Nature 356:37-41(1992).

RN [2]

RP REVISIONS.

RC STRAIN=BRISTOL N2;

RA Durbin R.;

RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).

CC -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.

CC

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

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CC or send an email to license@isb-sib.ch).

CC

DR EMBL; Z11115; CAA77460.1; -.

DR EMBL; Z22175; CAA77460.1; JOINED.

DR EMBL; Z22175; CAA80131.1; -.

DR EMBL; Z11115; CAA80131.1; JOINED.

DR PIR; S15786; S15786.

DR WormPep; ZK637.1; CE06638.

DR InterPro; IPR003662; sub_transporter.

DR Pfam; PF00083; sugar_tr; 1.

DR PROSITE; PS00216; SUGAR_TRANSPORT_1; FALSE_NEG.

DR PROSITE; PS00217; SUGAR_TRANSPORT_2; FALSE_NEG.

KW Hypothetical protein; Transmembrane; Transport.

FT DOMAIN 1 85 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	86	106	1 (POTENTIAL).
FT	DOMAIN	107	120	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	121	141	2 (POTENTIAL).
FT	DOMAIN	142	157	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	158	178	3 (POTENTIAL).
FT	DOMAIN	179	179	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	180	200	4 (POTENTIAL).
FT	DOMAIN	201	208	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	209	229	5 (POTENTIAL).
FT	DOMAIN	230	237	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	238	258	6 (POTENTIAL).
FT	DOMAIN	259	319	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	320	340	7 (POTENTIAL).
FT	DOMAIN	341	372	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	373	393	8 (POTENTIAL).
FT	DOMAIN	394	410	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	411	431	9 (POTENTIAL).
FT	DOMAIN	432	434	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	435	455	10 (POTENTIAL).
FT	DOMAIN	456	461	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	462	480	11 (POTENTIAL).
FT	DOMAIN	481	482	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	483	502	12 (POTENTIAL).
FT	DOMAIN	503	529	CYTOPLASMIC (POTENTIAL).
SQ	SEQUENCE	529 AA;	58317 MW;	8D2FF4CBA15ECD2D CRC64;

Query Match 13.2%; Score 387; DB 1; Length 529;
 Best Local Similarity 25.9%; Pred. No. 5.6e-22;
 Matches 128; Conservative 80; Mismatches 205; Indels 82; Gaps 15;

Qy	64	EVWLPRDRQGQPESCLRFTSPQWGLPFLNGTEANGTGTATEPCTD-----GWIYDN----- 113
Db	51	ELGEPTD-QRSPDSEKTFTVDE-----AVEALGFGRFQLKLSILTGMAMADAMEMML 102
Qy	114	-STFPSTIVTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLA DRLGRRKVLLNLYLQT 172
Db	103	LSLISPALACEWGISSVQQA--LVTTCVFSGMMLSSTFWGKICDRFGRRKGLTFSTLVA 159
Qy	173	AVSGTCAAFAFPNFPIYCAFRLLSGMALAGISLN CMTLNVEMPIHTRACVGTIGYVYSL 232
Db	160	CIMGVISGMSPHFYVLLFFRGLTGIGGVP-QSVTLYAEFLPTAQRAKCVVLIESFWAI 218
Qy	233	GQFLLAGVAYAVPH--WRHLQLLVSA PFAFFIYSWFFIESARWHSSGRLDLTLRQL 289
Db	219	GAVFEALLAYFVMESFGWRALMFLSSLPLGIFAVASFWLPESARFDMASGHPERALETLQ 278
Qy	290	RVARINGKREEGAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHFLCLSMWFAT 349
Db	279	AAARMN-----RVQLPTGRLVSSTKAGSESRGDIANLLSPDLRKTTILLWCIWAIT 329
Qy	350	SFAYYGLVM-----D LQFGGVSIYLIQVIFGA-----VDLPAKLVG 385
Db	330	AFSYYGMVLFTTVLFQSHDECHGGLFSNGTQMEVCQPLTRSDYFDLLSTTLAEFPGLIIT 389
Qy	386	FLVINSLGRRPAQMAALLAGI-----CILLNGVIPQDQSIVRTSLAVLGKGCLAASF 438
Db	390	VLIIEWFGRKKTMALEYAVFAIFTFLYFCL-----DRFTV-TV LIFVARAFISGAF 440
Qy	439	NCIFLYTGE LYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAELYPSPMLFIYGA VPVAAS 498
Db	441	QCAYVYTPEVYPTTLRAVGLGTCSAMARIGAIVASEKSL-----SLPIGIYGTAAI LGL 494
Qy	499	AVTVLLP-ETLGQPL 512
Db	495	IASLSPPIETKGROM 509

SUMMARIES

Result	Query
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No.	Score	Match	Length	DB	ID	Description
1	2924	100.0	563	4	O95742	O95742 homo sapien
2	2675	91.5	519	4	Q9NQA6	Q9nqa6 homo sapien
3	2583.5	88.4	506	4	Q9NQC2	Q9nqc2 homo sapien
4	2571	87.9	551	6	Q9TSY7	Q9tsy7 oryctolagus
5	2543	87.0	551	11	O35956	O35956 rattus norv
6	2443	83.5	545	11	Q61185	Q61185 mus musculu
7	1411.5	48.3	562	13	O57379	O57379 pseudopleur
8	1409.5	48.2	542	4	Q96TC1	Q96tc1 homo sapien
9	1376.5	47.1	537	11	O88909	O88909 mus musculu
10	1376.5	47.1	537	11	Q91WJ9	Q91wj9 mus musculu
11	1366.5	46.7	536	11	Q9R1U7	Q9r1u7 rattus norv
12	1267.5	43.3	553	11	O54778	O54778 mus musculu
13	1225.5	41.9	553	4	Q96S37	Q96s37 homo sapien
14	1204.5	41.2	568	4	O95820	O95820 homo sapien
15	1127	38.5	550	4	Q9NSA0	Q9nsa0 homo sapien

RESULT 1

O95742

ID O95742 PRELIMINARY; PRT; 563 AA.
 AC O95742; O95187; Q9UEQ8; Q9UBG6;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE RENAL ORGANIC ANION TRANSPORT PROTEIN 1.
 GN SLC22A6 OR OAT1 OR ROAT1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC TISSUE=KIDNEY;
 RX MEDLINE=99103997; PubMed=9887087;
 RA Hosoyamada M., Sekine T., Kanaai Y., Endou H.;
 RT "Molecular cloning and functional expression of a multispecific
 organic anion transporter from human kidney.";
 RL Am. J. Physiol. 276:F122-F128(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98433806; PubMed=9762842;
 RA Reid G., Wolff N.A., Dautzenberg F.M., Burckhardt G.;
 RT "Cloning of a human renal p-aminohippurate transporter, hROAT1.";
 RL Kidney Blood Press. Res. 21:233-237(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE=99137667; PubMed=9950961;
 RA Lu R., Chan B.S., Schuster V.L.;
 RT "Cloning of the human kidney PAH transporter: narrow substrate
 specificity and regulation by protein kinase C.";
 RL Am. J. Physiol. 276:F295-F303(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE=99160894; PubMed=10049739;
 RA Race J.E., Grassl S.M., Williams W.J., Holtzman E.J.;
 RT "Molecular cloning and characterization of two novel human renal
 organic anion transporters (hOAT1 and hOAT3)." ;
 RL Biochem. Biophys. Res. Commun. 255:508-514(1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RX MEDLINE=99393620; PubMed=10462545;
 RA Cihlar T., Lin D.C., Pritchard J.B., Fuller M.D., Mendel D.B.,
 RA Sweet D.H.;
 RT "The antiviral nucleotide analogs cidofovir and adefovir are novel
 substrates for human and rat renal organic anion transporter 1.";

RL Mol. Pharmacol. 56:570-580(1999).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Bahn A., Prawitt D., Reid G., Enklaar T., Wolff N.A., Hillemann A.,
 RA Godehardt S., Buttler D., Knabe M., Schulten H.J., Gunawan B.,
 RA Fuezesi L., Zabel B., Burckhardt G.;
 RT "Genomic cloning and characterization of the human renal organic anion
 transporter gene (hOAT1).";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: MEDIATES THE NA(+) -INDEPENDENT TRANSPORT OF ORGANIC
 CC ANIONS SUCH AS P-AMINOHIPPURATE AND ALPHA-KETOGlutARATE.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. BASOLATERAL
 CC MEMBRANE (POTENTIAL).
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ISOFORM HOAT1-1 (SHOWN HERE)
 CC AND ISOFORM HOAT1-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN KIDNEY. ALSO DETECTED IN
 CC BRAIN AND AT LOW LEVELS, IN SKELETAL MUSCLE AND PLACENTA. NOT
 CC EXPRESSED IN HEART, LUNG, LIVER, PANCREAS, COLON, THYMUS, SMALL
 CC INTESTINE OR PERIPHERAL BLOOD LEUKOCYTES. IN THE KIDNEY, STRONGLY
 CC EXPRESSED IN PROXIMAL TUBULE CELLS.
 CC -!- PTM: GLYCOSYLATED.
 CC -!- SIMILARITY: BELONGS TO THE SLC22 FAMILY OF TRANSPORTERS.
 DR EMBL; AF057039; AAC70004.1; -.
 DR EMBL; AB009697; BAA75072.1; -.
 DR EMBL; AF104038; AAD10052.1; -.
 DR EMBL; AB009698; BAA75073.1; -.
 DR EMBL; AF097490; AAD19356.1; -.
 DR EMBL; AF124373; AAD55356.1; -.
 DR EMBL; AJ249369; CAB77184.1; -.
 DR InterPro; IPR003662; sub_transporter.
 DR Pfam; PF00083; sugar_tr; 1.
 KW Transmembrane; Transport; Alternative splicing; Ion transport;
 KW Glycoprotein.
 FT TRANSMEM 136 156 POTENTIAL.
 FT TRANSMEM 185 205 POTENTIAL.
 FT TRANSMEM 249 269 POTENTIAL.
 FT TRANSMEM 338 358 POTENTIAL.
 FT TRANSMEM 396 416 POTENTIAL.
 FT TRANSMEM 426 446 POTENTIAL.
 FT TRANSMEM 485 505 POTENTIAL.
 FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPlic 523 535 MISSING (IN ISOFORM OAT1.2).
 FT CONFLICT 14 14 G -> S (IN REF. 3).
 FT CONFLICT 563 563 L -> F (IN REF. 2).
 SQ SEQUENCE 563 AA; 61816 MW; 74AD3EA2678032E4 CRC64;

Query Match 100.0%; Score 2924; DB 4; Length 563;
 Best Local Similarity 100.0%; Pred. No. 1.9e-227;
 Matches 563; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MAFNDLLQQVGGVGRFQQIQVTLVVLPLLLMASHNTLQNFTAAIPTHHCRPPADANLSKN	60
Db	1 MAFNDLLQQVGGVGRFQQIQVTLVVLPLLLMASHNTLQNFTAAIPTHHCRPPADANLSKN	60
Qy	61 GGLEVWLPRDRQQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI	120
Db	61 GGLEVWLPRDRQQPESCLRFTSPQWGLPFLNGTEANGTGATEPCTDGWIYDNSTFPSTI	120
Qy	121 VTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNLYLQTAVSGTCAA	180
Db	121 VTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLILNLYLQTAVSGTCAA	180
Qy	181 FAPNFPPIYCAFRLLSGMALAGISLNCMTLNVEWMP1HTRACVGTLIGYVYSLQFLLAGV	240
Db	181 FAPNFPPIYCAFRLLSGMALAGISLNCMTLNVEWMP1HTRACVGTLIGYVYSLQFLLAGV	240

Qy 241 AYAVPHWRHLQLLVSAFFIYSWFFIESARWHSSGRDLTLRALQRVARINGKREE 300
 |||||
 Db 241 AYAVPHWRHLQLLVSAFFIYSWFFIESARWHSSGRDLTLRALQRVARINGKREE 300
 |||||
 Qy 301 GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMWFATSFAYYGLVMDL 360
 |||||
 Db 301 GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMWFATSFAYYGLVMDL 360
 |||||
 Qy 361 QGFGVSIYLIQVIFGAVDLPALKVGLVINSLGRRPAQMAALLLAGICILLNGVIPQDQS 420
 |||||
 Db 361 QGFGVSIYLIQVIFGAVDLPALKVGLVINSLGRRPAQMAALLLAGICILLNGVIPQDQS 420
 |||||
 Qy 421 IVRTSLAVLGKGCLAAASFNCIFLYTGELEYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480
 |||||
 Db 421 IVRTSLAVLGKGCLAAASFNCIFLYTGELEYPTMIRQTGMGMGSTMARVGSIVSPLVSMTAE 480
 |||||
 Qy 481 LYPSTMPLFIYGAVPVAASAVTVLLPETLGQPLPDTVQDLESRWAPTQKEAGIYPRKGKQT 540
 |||||
 Db 481 LYPSTMPLFIYGAVPVAASAVTVLLPETLGQPLPDTVQDLESRWAPTQKEAGIYPRKGKQT 540
 |||||
 Qy 541 RQQQEHQKYMVPLQASAQEKNGL 563
 |||||
 Db 541 RQQQEHQKYMVPLQASAQEKNGL 563

RESULT 5
 035956
 ID 035956 PRELIMINARY; PRT; 551 AA.
 AC 035956;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE RENAL ORGANIC ANION TRANSPORT PROTEIN 1.
 GN SLC22A6 OR ROAT1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC TISSUE=KIDNEY;
 RX MEDLINE=98043701; PubMed=9374486;
 RA Sweet D.H., Wolff N.A., Pritchard J.B.;
 RT "Expression cloning and characterization of ROAT1. The basolateral
 RT organic anion transporter in rat kidney.";
 RL J. Biol. Chem. 272:30088-30095(1997).
 RN [2]
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;
 RX MEDLINE=97373539; PubMed=9228014;
 RA Sekine T., Watanabe N., Hosoyamada M., Kanai Y., Endou H.;
 RT "Expression cloning and characterization of a novel multispecific
 RT organic anion transporter.";
 RL J. Biol. Chem. 272:18526-18529(1997).
 CC -!- FUNCTION: MEDIATES THE NA(+) -INDEPENDENT TRANSPORT OF ORGANIC
 CC ANIONS SUCH AS CYCLIC NUCLEOTIDES, PROSTAGLANDIN E2 AND URIC ACID.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. BASOLATERAL
 CC MEMBRANE (POTENTIAL).
 CC -!- TISSUE SPECIFICITY: STRONG EXPRESSION IN KIDNEY. VERY WEAK
 CC EXPRESSION IN BRAIN. NOT DETECTED IN HEART, LUNG, LIVER, SPLEEN
 CC SKELETAL MUSCLE, SMALL INTESTINE, LARGE INTESTINE, EYE OR TESTIS.
 CC EXPRESSED IN THE PROXIMAL TUBULE IN THE KIDNEY.
 CC -!- PTM: GLYCOSYLATED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SLC22 FAMILY OF TRANSPORTERS.
 DR EMBL; AF008221; AAC18772.1; -.
 DR EMBL; AB004559; BAA22086.1; -.
 DR InterPro; IPR003662; sub_transporter.
 DR Pfam; PF00083; sugar_tr; 1.
 KW Transmembrane; Transport; Glycoprotein; Ion transport.
 FT TRANSMEM 136 156 POTENTIAL.

FT	TRANSMEM	196	216	POTENTIAL.
FT	TRANSMEM	249	269	POTENTIAL.
FT	TRANSMEM	338	358	POTENTIAL.
FT	TRANSMEM	396	416	POTENTIAL.
FT	TRANSMEM	485	505	POTENTIAL.
FT	CARBOHYD	39	39	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	56	56	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	92	92	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	97	97	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	113	113	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	184	184	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	551 AA;	60766 MW;	8BA47BE628324BF2 CRC64;

Query Match 87.0%; Score 2543; DB 11; Length 551;
 Best Local Similarity 86.0%; Pred. No. 9.5e-197;
 Matches 484; Conservative 35; Mismatches 32; Indels 12; Gaps 1;

Qy	1	MAFN DLLQQVGGVGRFQQIQVTLVLPPLLMA SHNTLQNF TAAI PTHHCRPPADANLSKN	60
Db	1	MAFN DLLKQVGGVGRFQLIQVTMVA PPLLMA SHNTLQNF TAAI PPHHCRPPADANLSKD	60
Qy	61	GGLEVWLPDRQGPESCLRFTSPQWGLPFLNGTEANGT GATEPCTDGWIYDNSTFPSTI	120
Db	61	GGLEAWLPPLDKQGPESCLRFTSPQWGPFFYNGTEANGTRVTEPCIDGWVYDNSTFPSTI	120
Qy	121	VTEWDLVCSH RALRQLAQSLYMGVLLGAMVFGYLADRLGRRKV LILNLYLQTA VSGTCAA	180
Db	121	VTEWNLVCSH RALRQLAQSLYMGVLLGAMVFGYLADRLGRRKV LILNLYLQTA VSGTCAA	180
Qy	181	FAPNFP IYCAF RLLSGM ALAGISL NCMLN VEWMP IHT RACVG TLIGYV YSLGQFLLAGV	240
Db	181	YAPNYT VYCVF RLLSGM SLASIA INCMLN VEWMP IHT RAYVG TLIGYV YSLGQFLLAGI	240
Qy	241	AYAVPHW RHLQLL VSAPF AFFI YSWFFIESARW HSSSGR LDTL RALQ RVARINGKREE	300
Db	241	AYAVPHW RHLQLV SVPFFIAFI YSWFFIESARW HSSSGR LDTL RALQ RVARINGKQEE	300
Qy	301	GAKLSM EVL RASL QKEL TMKG QASAME LLRCPTL RHLFLCLSM LWFAT SFAY YGLVMDL	360
Db	301	GAKLSIEV LRTS LQKEL TSKG QASAME LLRCPTL RHLFLCLSM LWFAT SFAY YGLVMDL	360
Qy	361	QGFGV SIYLIQV IFGAVD LPAKLV GFLV INSLG RRPAQMA ALLL AGIC ILLNGV IPQDQS	420
Db	361	QGFGV S MYLIQV IFGAVD LPAKF VCLV INSMG RRPAQMAS LLLAGIC I L VNGI IPKSHT	420
Qy	421	IVRTSLA VLKG GCLAA SFNC IFLY TGELY PTMIR QTGM GMGST MARV GSIV SPLV SMTAE	480
Db	421	IIRTS LAVL KGCLASS FNC IFLY TGELY PTVIR QTGL GMGST MARV GSIV SPLV SMTAE	480
Qy	481	LYPSMPLFIYGA VPVA ASAVT VLLP ETLG QPLP DTVQ DLES RWAPT QKEAGI YPRKGK QT	540
Db	481	FYPSMPLF IFGAVP VV ASAVT ALLP ETLG QPLP DTVQ DLSR----- SRGKQ N	528
Qy	541	RQQQE HQKYM VPQ ASAQ EK NGL	563
Db	529	QQQQE QQKQ MMPLQ ASQ EK NGL	551

RESULT	6			
Q61185				
ID	Q61185	PRELIMINARY;	PRT;	545 AA.
AC	Q61185;			
DT	01-NOV-1996	(TrEMBLrel. 01, Created)		
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)		
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)		
DE	KIDNEY-SPECIFIC TRANSPORT PROTEIN.			
GN	SLC22A6.			
OS	Mus musculus (Mouse).			

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=97197822; PubMed=9045672;
 RA Lopez-Nieto C.E., You G., Bush K.T., Barros E.J., Beier D.R.,
 RA Nigam S.K.;
 RT "Molecular cloning and characterization of NKT, a gene product related
 RT to the organic cation transporter family that is almost exclusively
 RT expressed in the kidney.";
 RL J. Biol. Chem. 272:6471-6478(1997).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
 DR EMBL; U52842; AAC53112.1; -.
 DR MGD; MGI:892001; Slc22a6.
 DR InterPro; IPR003662; sub_transporter.
 DR Pfam; PF00083; sugar_tr; 1.
 KW Transmembrane.
 SQ SEQUENCE 545 AA; 59983 MW; CD3B762E5984933A CRC64;

Query Match 83.5%; Score 2443; DB 11; Length 545;
 Best Local Similarity 83.1%; Pred. No. 1.1e-188;
 Matches 468; Conservative 41; Mismatches 36; Indels 18; Gaps 2;

Qy	1 MAFNDLLQQVGGVGRFQQIQVTLVLPPLLMAHNTLQNFTAAIPTHHCRPPADANLSKN 60
	: : : :
Db	1 MAFNDLLKQVGGVGRFQLIQVTMVAAPLLLMAHNTLQNFTAAIPAHHCRPPANANLSKD 60
Qy	61 GGLEVWLPRDRQGPESCLRFTSPQWGLPFLNGTEANGTGatePCTDGWIYDNSTFPSTI 120
	: : : : : : : : : :
Db	61 GGLEARLPLDKQGRPESCLRFPFPH-----NGTEANGTGVTEPCLDGWVYDNSTFPSTI 114
Qy	121 VTEWDLVCSHRALRQLAQSLYMGVLLGAMVFGYLADRLGRRKVLLNLYLQTAVSGTC 180
	: : : : : : : : :
Db	115 VTEWNLVCSHRAFRQLAQSLFMVGVLLGAMMFGYLADRLGRRKVLLNLYLQTAVSGTC 174
Qy	181 FAPNPFPIYCAFRLLSGMALAGISLNCMTLNVEWMPHIHTRACVGTLLIGYVYSLQFLL 240
	: : : : : : : : : : : : : :
Db	175 YAPNYTVYCIFRLLSGMSLASIAINCMTLNMEWMPHIHTRAYVGTLLIGYVYSLQFLL 234
Qy	241 AYAVPHWRHLQLLVSAFPFAFFIYSWFFIESARWHSSGRDLTLRALQRVARINGKREE 300
	: : : : : : : : : :
Db	235 AYAVPHWRHLQLAVSVPFFVAIFIYSWFFIESARWYSSSGRDLTLRALQRVARINGKQEE 294
Qy	301 GAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRLFLCLSMWFATSFAYYGLVMDL 360
	: : : : : : : : :
Db	295 GAKLSIEVLQTSLQKELTLNKGQASAMELLRCPTLRLFLCLSMWFATSFAYYGLVMDL 354
Qy	361 QGFGVSIYLIQVIFGAVDLPACKLVGLVINSLGRRPAQMAALLLAGICILLNGVI 420
	: : : : : : : : :
Db	355 QGFGVSMYLIQVIFGAVDLPACKFVCLVINSMGRRPAQLASLLLALGICILVNGII 414
Qy	421 IVRTSLAVLGKGCLAAFNCFIYLYTGELEYPTMIOTGMGMGSTMARVGSIVSPLVSM 480
	: : : : : : : : : : : : : :
Db	415 IIRTSVLAVLGKGCLASSFNCFIYLYTGELEYPTMIRQTGLGMGSTMARVGSIVSPL 474
Qy	481 LYPSMPLFIYGAAPVAASAVTLLPETYLGQPLPDTVQDLESRWAPTQKEAGIYPRKGKQT 540
	: : : : : : : : : : : : :
Db	475 FYPSPPLFIFGAVPVAASAVTALLPETYLGQPLPDTVQDLKSR-----SRGKQK 522
Qy	541 RQQQEHQKYMVPLQASAQEKNGL 563
	: :
Db	523 QQGLEQQKQMIPLQVSTQEKNGL 545

057379 PRELIMINARY; PRT; 562 AA.

AC 057379;

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE RENAL ORGANIC ANION TRANSPORTER.

OS Pseudopleuronecta americanus (Winter flounder).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

OC Pleuronectoidei; Pleuronectidae; Pseudopleuronectes.

OX NCBI_TaxID=8265;

RN [1]

RP SEQUENCE FROM N.A., AND FUNCTION.

RC TISSUE=KIDNEY;

RX MEDLINE=98072393; PubMed=9409735;

RA Wolff N.A., Werner A., Burkhardt S., Burckhardt G.;

RT "Expression cloning and characterization of a renal organic anion transporter from winter flounder.";

RL FEBS Lett. 417:287-291(1997).

CC -!- FUNCTION: MEDIATES THE NA(+) -INDEPENDENT TRANSPORT OF ORGANIC ANIONS SUCH AS P-AMINOHIPPURATE.

CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. BASOLATERAL MEMBRANE (POTENTIAL).

CC -!- PTM: GLYCOSYLATED (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE SLC21 FAMILY OF TRANSPORTERS.

DR EMBL; Z97028; CAB09724.1; -.

DR InterPro; IPR003662; sub_transporter.

DR Pfam; PF00083; sugar_tr; 1.

KW Transmembrane; Transport; Glycoprotein; Ion transport.

FT TRANSMEM 148 168 POTENTIAL.

FT TRANSMEM 175 195 POTENTIAL.

FT TRANSMEM 206 226 POTENTIAL.

FT TRANSMEM 261 281 POTENTIAL.

FT TRANSMEM 409 429 POTENTIAL.

FT TRANSMEM 496 516 POTENTIAL.

FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 562 AA; 61992 MW; 7DC1A67F32801D2D CRC64;

Query Match 48.3%; Score 1411.5; DB 13; Length 562;
Best Local Similarity 48.6%; Pred. No. 1.6e-105;
Matches 270; Conservative 109; Mismatches 155; Indels 21; Gaps 4;

Qy	1	MAFNDDLLQQVGGVGRFQQIQVTLLVVLPLLLMASHNTLQNFATAPTHHCRPPAD--ANL	57
Db	1	MPFSELLEQVGSTGRFQVLHVTLCLPVLMMASHNLNQNFATVPSHYCNAHANLSQARL	60
Qy	58	SKNGGLEEVWLPRDRQGPESCLRFTSPQWGLPFLNGTEANG-----TGATEPCTDG	108
Db	61	SLEESLLITVPLDGAGKPQRCQRYAAPQWHLLGKNGTSGSGDLADATESMDAALQECSDG	120
Qy	109	WIYDNSTFPSTIVTEWDLVCNSHRALRQLAQSLYMGVLLGAMVFGYLADRLLGRRKVILN	168
Db	121	WSYNSTVRSSTIISEWHLVCDMHFSFKQMGQTIIYMGGLVGALLFGGLSDRYGRRILLIS	180
Qy	169	YLQTAVSGTCAAFAFPNFIYCAFRLLSGMALAGISLNCTLNVEWMPIHTRACVGTLLIGY	228
Db	181	NLLMAVSGTCAAFFSSFSLFCVFRFGCGLALSGLGLNTFSLIVEWIPTRIRTAVGTTGY	240
Qy	229	VYSLGQFLLAGVAYAVPHWRHLQLLVSAPFFAFIYISWFFIESARWHSSSGRLDRTLAL	288
Db	241	CYTLGQLILVLLAYFIRDWRWLTLAVSLPFIYVFLIAWWFHESSRWLALSNRTEHALKNL	300
Qy	289	QRVARARINGKREEGAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRLHFLCLMSLWFA	348
Db	301	KSVARFNGRHEEAELDIKMLHESMKMECTQGSYSILDLFNTPAMRKRTLCLSAVWLS	360

Qy	349	TSFAYYGLVMDLQFGVSIYLIQVIFGAVDLPALKVGLVINSLGRPAQMAALLAGIC	408
		: : : : : :	
Db	361	TSFAYYGLAMDLDFGVDIYLIQVIFGAVDIPAKVVVVVMSLIGRRRSQCAVLVVAGIT	420
		: : : : : : :	
Qy	409	ILLNGVIPQDQSIVRTSLAVLGKGLAASFNCIFLYTGELYPTMIRQTGMGMGSTMARVG	468
		: : : : : : : :	
Db	421	ILLNLVVYPDKQTIRTCALVLGKGLAASFNCYLYSGELFPTIIRQNGMGWVSMMARIG	480
		: : : : : : : : : : : : : : :	
Qy	469	SIVSPLVSMTAELYPSMPLFIFYGAVPVAASAVTVLLPETLGQQLPDTVQDLESRWAPTQK	528
		::: : : : : : : : : : : : : : : :	
Db	481	AMVAPMVLLTRDYIPWLPGLIYGGAPILSGLAAIFLPETLGYPPLPDTIQDVE-----	532

Qy	529	EAGIYPRKGKQTRQQ	543
		: : : :	
Db	533	ESG-SGRKSKMSTKE	546

RESULT 12
054778
ID 054778 PRELIMINARY; PRT; 553 AA.
AC 054778;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE RST.
GN SLC22AL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=98072412; PubMed=9409754;
RA Mori K., Ogawa Y., Ebihara K., Aoki T., Tamura N., Sugawara A.,
RA Kuwahara T., Ozaki S., Mukoyama M., Tashiro K., Tanaka I., Nakao K.;
RT "Kidney-specific expression of a novel mouse organic cation
RT transporter-like protein.";
RL FEBS Lett. 417:371-374(1997).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
DR EMBL; AB005451; BAA23875.1; -.
DR MGD; MGI:1195269; Slc22a12.
DR InterPro; IPR003662; sub_transporter.
DR Pfam; PF00083; sugar_tr; 1.
KW Transmembrane.
SQ SEQUENCE 553 AA; 60160 MW; D991F5F74A39BBBF CRC64;

Query Match 43.3%; Score 1267.5; DB 11; Length 553;
Best Local Similarity 46.9%; Pred. No. 6.5e-94;
Matches 250; Conservative 91; Mismatches 181; Indels 11; Gaps 3;

Qy	1	MAFNDDLQQVGGVGRFQQIQVTLVVLPPLLMAHNTLQNFTAAIPTHHCRPP-----AD	54
		: : : : : : : : : : : : : : : :	
Db	1	MAFPELLDRVGGLGRFQLFQTVLVTPILWVTTQNMLENFSAAPVHRCWVPLLDNSTSQ	60
Qy	55	ANLSKNGG---LEVWLPRDRQGQPESCLRFTSPQWGLPFLNGTEAN-GTGATEPCTDGW	109
:	:	: : : : : : : : : : : : : : : : : : :	:
Db	61	ASIPGDLGPDVLLAVSIPPGPDQQPHQCLRFRQPWQLTESNATATNWSDAATEPCEDGW	120
Qy	110	IYDNSTFPSTIVTEWDLVCSHRALRQLAQSLYMGVGLGAMVFGYLADRLGRRKVLI	169
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Db	121	VYDHSTFRSTIVTTWDLVCNSQALRPMQAQSIFLAGILVGAAVCGHASDRFGRRRVLTWSY	180
Qy	170	LQTAVGSGTCAAFAPNPFPIYCAFRLLSGMALAGISLNCMTLNVEWMPITHRACVGT	229
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Db	181	LLVSVSGTAAAFMPTFLYCLFRFLLASAVAGVMMNTASLLMEWTSAQGSPLVMTLNALG	240
Qy	230	YSLGQFLLAGVAYAVPHWRHLQLLVSAPFFAFFIYSWFFIESARWHSSSGRIDLTLRALQ	289

Db 241 FSFGQVLTGSVAYGVRSWRMLQLAVSAPFFLFFFVYSWLPESARWLITVGKLDQGLQELQ 300
Qy 290 RVARINGKREEGAKLSMEVLRASLQKELTMGKGQASAMELLRCPTLRHLFLCLSMWFAT 349
Db 301 RVAAVNRKAEGLDTLTMEVLRSAMEEEPSRDKAGASLGTLHPTGLRHRTIISMLCWFAF 360
Qy 350 SFAYYGLVMDLQGFGVSIYLIQVIFGAVDLPALKVGLVINSLGRRPAQMAALLLAGICI 409
Db 361 GFTFYGLALDLQALGSNIFLLQALIGIVDFPVKTGSLLLISRLGRRLCQVSFLVPLGLCI 420
Qy 410 LLNGVIPQDQSIVRTSLAVLGKGCLAAASFNCIFLYTGEELYPTMIRQTGMGMGSTMARVGS 469
Db 421 LSNILVPHGMGVLRSLAVALGLGCLGGAFTCITIFSSELFPTVIRMTAVGLCQVAARGGA 480
Qy 470 IVSPLVSMTAELYPSMPLFIYGAJVVAASAVTVLLPETLGQPLPDTVQDLESR 522
Db 481 MLGPLVRLLGVYGSWMPPLLVYGVVPVLSGLAALLLPETKNLPLPDTIQDIQKQ 533